

## SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Somerville, Chris  
Broun, Pierre  
van de Loo, Frank  
Boddupalli, Sekhar S.

(ii) ~~TITLE OF INVENTION:~~ Production of Hydroxylated Fatty Acids in Genetically Modified Plants

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: PILLSBURY MADISON & SUTRO  
(B) STREET: 1100 NEW YORK AVENUE, N.W.  
(C) CITY: WASHINGTON  
(D) STATE: D.C.  
(E) COUNTRY: USA  
(F) ZIP: 20005-3918

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 MB storage  
(B) COMPUTER: IBM compatible  
(C) OPERATING SYSTEM: DOS 5.0  
(D) SOFTWARE: Word Perfect 5.1

(vi) CURRENT APPLICATION DATA;

(A) APPLICATION NUMBER: not yet assigned  
(B) FILING DATE: February 6, 1997  
(C) CLASSIFICATION:

(2) INFORMATION FOR SEQ ID NO:1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 543 nucleotides  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TATTGGCACC	GGCGGCACCA	TTCGAACAAT	GGATCCCTAG	40
AAAAAGATGA	AGTCTTTGTC	CCACCTAAGA	AAGCTGCAGT	80
CANATGGTAT	GTCAAATACC	TCAACAACCC	TCTTGGACGC	120
ATTCTGGTGT	TAACAGTTCA	GTTTATCCTC	GGGTGGCCTT	160

[illegible]

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TGTATCTAGC CTTTAATGTA TCAGGTAGAC CTTATGATGG 200  
 TTTCGCTTCA CATTCTCTCC CTCATGCACC TATCTTTAAG 240  
 GACCGTGAAC GTCTCCAGAT ATACATCTCA GATGCTGGTA 280  
 TTCTAGCTGT CTGTTATGGT CTTTACCGTT ACGCTGCTTC 320  
 ACAAGGATTG ACTGCTATGA TCTGCGTCTA CGGAGTACCG 360  
 CTTTGTGATAG TGAACCTTTT CTTGTCTTG GTCACCTTCT 400  
 TGCAGCACAC TCATCCTTCA TTACCTCACT ATGATTCAAC 440  
 CGAGTGGGAA TGGATTAGAG GAGCTTTGGT TACGGTAGAC 480  
 AGAGACTATG GAATCTTGAA CAAGGTGTTT CACAACATAA 520  
 CAGACACCCA CGTAGCACAC CAC 543

(2) INFORMATION FOR SEQ ID NO:2

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 544 nucleotides
  - (B) TYPE: nucleotide
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TATAGGCACC GGAGGCACCA TTCCAACACA GGATCCCTCG 40  
 AAAGAGATGA AGTATTTGTC CCAAAGCAGA AATCCGCAAT 80  
 CAAGTGGTAC GCGGAATACC TCAACAACCC TCCTGGTCGC 120  
 ATCATGATGT TAACTGTCCA GTTCGTCTCTC GGATGGCCCT 160  
 TGTACTIONAGC CTTCAACGTT TCTGGCAGAC CCTACAATGG 200  
 TTTCGCTTCC CATTCTCTCC CCAATGCTCC TATCTACAAC 240  
 GACCGTGAAC GCCTCCAGAT TTACATCTCT GATGCTGGTA 280  
 TTCTAGCCGT CTGTTATGGT CTTTACCGTT ACGCTGTTGC 320  
 ACAAGGACTA GCCTCAATGA TCTGTCTAAA CGGAGTTCCG 360  
 CTTCTGATAG TTAACCTTTT CTCGTCTTG ATCACTTACT 400

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cont

TACAACACAC TCACCCTGCG TTGCCTCACT ATGATTCATC 440  
AGAGTGGGAT TGGCTTAGAG GAGCTTTAGC TACTGTAGAC 480  
AGAGACTATG GAATCTTGAA CAAGGTGTTC CATAACATCA 520  
CAGACACCCA CGTCGCACAC CACT 544

(2) INFORMATION FOR SEQ ID NO:3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1855 nucleotides
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGAAGCTTT ATAAGAAGTT AGTTTTCTCT GGTGACAGAG 40  
AAATTNTGTC AATTGGTAGT GACAGTTGAA GCAACAGGAA 80  
CAACAAGGAT GGTGTTGNT GATGCTGATG TGGTGATGTG 120  
TTATTCATCA AATACTAAAT ACTACATTAC TTGTTGCTGC 160  
CTACTTCTCC TATTTCTCC GCCACCCATT TTGGACCCAC 200  
GANCCTTCCA TTAAACCCT CTCTCGTGCT ATTCACCAGA 240  
AGAGAAGCCA AGAGAGAGAG AGAGAGAATG TTCTGAGGAT 280  
CATTGTCTTC TTCATCGTTA TTAACGTAAG TTTTTTTTGA 320  
CCACTCATAT CTAAAATCTA GTACATGCAA TAGATTAATG 360  
ACTGTTCTTT CTTTGTATAT TTTGAGCTTC TTGAATTCAA 400  
GATGGGTGCT GGTGGAAGAA TAATGGTTAC CCCCTCTTCC 440  
AAGAAATCAG AAAGTGAAGC CCTAAAACGT GGACCATGTG 480  
AGAAACCACC ATTCAGTGT AAAGATCTGA AGAAAGCAAT 520  
CCCACAGCAT TGTTTCAAGC GCTCTATCCC TCGTTCTTTC 560  
TCCTACCTTC TCACAGATAT CACTTTAGTT TCTTGCTTCT 600  
ACTACGTTGC CACAAATTAC TTCTCTCTTC TTCCTCAGCC 640

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cont

TCTCTCTACT TACCTAGCTT GGCCTCTCTA TTGGGTATGT 680  
CAAGGCTGTG TCTTAACCGG TATCTGGGTC ATTGGCCATG 720  
AATGTGGTCA CCATGCATTC AGTGA CTATC AATGGGTAGA 760  
TGACACTGTT GGTTTTATCT TCCATTCCCTT CCTTCTCGTC 800  
CCTTACTTCT CCTGGAAATA CAGTCATCGT CGTCACCATT 840  
CCAACAATGG ATCTCTCGAG AAAGATGAAG TCTTTGTCCC 880  
ACCGAAGAAA GCTGCAGTCA AATGGTATGT TAAATACCTC 920  
AACCAACCCTC TTGGACGCAT TCTGGTGTTA ACAGTTCAGT 960  
TTATCCTCGG GTGGCCTTTG TATCTAGCCT TTAATGTATC 1000  
AGGTAGACCT TATGATGGTT TCGCTTCACA TTTCTTCCCT 1040  
CATGCACCTA TCTTTAAAGA CCGAGAACGC CTCCAGATAT 1080  
ACATCTCAGA TGCTGGTATT CTAGCTGTCT GTTATGGTCT 1120  
TTACCGTTAC GCTGCTTCAC AAGGATTGAC TGCTATGATC 1160  
TGCGTCTATG GAGTACCGCT TTTGATAGTG AACTTTTTCC 1200  
TTGTCTTGGT AACTTTCTTG CAGCACACTC ATCCTTCGTT 1240  
ACCTCATTAT GATTCAACCG AGTGGGAATG GATTAGAGGA 1280  
GCTTTGGTTA CGGTAGACAG AGACTATGGA ATATTGAACA 1320  
AGGTGTTCCA TAACATAACA GACACACATG TGGCTCATCA 1360  
TCTCTTTGCA ACTATACCGC ATTATAACGC AATGGAAGCT 1400  
ACAGAGGCGA TAAAGCCAAT ACTTGGTGAT TACTACCACT 1440  
TCGATGGAAC ACCGTGGTAT GTGGCCATGT ATAGGGAAGC 1480  
AAAGGAGTGT CTCTATGTAG AACCGGATAC GGAACGTGGG 1520  
AAGAAAGGTG TCTACTATTA CAACAATAAG TTATGAGGCT 1560  
GATAGGGCGA GAGAAGTGCA ATTATCAATC TTCATTTCCA 1600  
TGTTTTAGGT GTCTTGTTTA AGAAGCTATG CTTTGTTTCA 1640  
ATAATCTCAG AGTCCATNTA GTTGTGTTCT GGTGCATTTT 1680

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GCCTAGTTAT	GTGGTGTCGG	AAGTTAGTGT	TCAAAC TGCT	1720
TCCTGCTGTG	CTGCCCAGTG	AAGAACAAGT	TTACGTGTTT	1760
AAAATACTCG	GAACGAATTG	ACCACAA NAT	ATCCAAAACC	1800
GGCTATCCGA	ATTCCATATC	CGAAAACCGG	ATATCCAAAT	1840
TTCCAGAGTA	CTTAG			1855

(2) INFORMATION FOR SEQ ID NO:4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Ala Gly Gly Arg Ile Met Val Thr  
5 10

Pro Ser Ser Lys Lys / Ser Glu Thr Glu Ala  
15 20

Leu Lys Arg Gly Pro Cys Glu Lys Pro Pro  
25 30

Phe Thr Val Lys Asp Leu Lys Lys Ala Ile  
35 40

Pro Gln His Cys Phe Lys Arg Ser Ile Pro  
45 50

Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile  
55 60

Thr Leu Val Ser Cys Phe Tyr Tyr Val Ala  
65 70

Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro  
75 80

Leu Ser Thr Tyr Leu Ala Trp | Pro Leu Tyr  
85 90

Trp Val Cys Gln Gly Cys Val Leu Thr Gly  
95 100

Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

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Ile Trp Val Ile Gly His Glu Cys Gly His  
 105 110  
 His Ala Phe Ser Asp Tyr Gln Trp Val Asp  
 115 120  
 Asp Thr Val Gly Phe Ile Phe His Ser Phe  
 125 130  
 Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr  
 135 140  
 Ser His Arg Arg His His Ser Asn Asn Gly  
 145 150  
 Ser Leu Glu Lys Asp Glu Val Phe Val Pro  
 155 160  
 Pro Lys Lys Ala Ala Val Lys Trp Tyr Val  
 165 170  
 Lys Tyr Leu Asn Asn Pro Leu Gly Arg Ile  
 175 180  
 Leu Val Leu Thr Val Gln Phe Ile Leu Gly  
 185 190  
 Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser  
 195 200  
 Gly Arg Pro Tyr Asp Gly Phe Ala Ser His  
 205 210  
 Phe Phe Pro His Ala Pro Ile Phe Lys Asp  
 215 220  
 Arg Glu Arg Leu Gln Ile Tyr Ile Ser Asp  
 225 230  
 Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu  
 235 240  
 Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr  
 245 250  
 Ala Met Ile Cys Val Tyr Gly Val Pro Leu  
 255 260  
 Leu Ile Val Asn Phe Phe Leu Val Leu Val  
 265 270

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Thr Phe Leu Gln His Thr His Pro Ser Leu  
 275 280  
 Pro His Tyr Asp Ser Thr Glu Trp Glu Trp  
 285 290  
 Ile Arg Gly Ala Leu Val Thr Val Asp Arg  
 295 300  
 Asp Tyr Gly Ile Leu Asn Lys Val Phe His  
 305 310  
 Asn Ile Thr Asp Thr His Val Ala His His  
 315 320  
 Leu Phe Ala Thr Ile Pro His Tyr Asn Ala  
 325 330  
 Met Glu Ala Thr Glu Ala Ile Lys Pro Ile  
 335 340  
 Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr  
 345 350  
 Pro Trp Tyr Val Ala Met Tyr Arg Glu Ala  
 355 360  
 Lys Glu Cys Leu Tyr Val Glu Pro Asp Thr  
 365 370  
 Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr  
 375 380  
 Asn Asn Lys Leu

## (2) INFORMATION FOR SEQ ID NO:5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Gly Gly Gly Gly Arg Met Ser Thr Val  
 5 10  
 Ile Thr Ser Asn Asn Ser Glu Lys Lys Gly  
 15 20

Sub  
 A1  
 Cont.

Gly Ser Ser His Leu Lys Arg Ala Pro His  
 25 30  
 Thr Lys Pro Pro Phe Thr Leu Gly Asp Leu  
 35 40  
 Lys Arg Ala Ile Pro Pro His Cys Phe Glu  
 45 50  
 Arg Ser Phe Val Arg Ser Phe Ser Tyr Val  
 55 60  
 Ala Tyr Asp Val Cys Leu Ser Phe Leu Phe  
 65 70  
 Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr  
 75 80  
 Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp  
 85 90  
 Leu Val Tyr Trp Leu Phe Gln Gly Cys Ile  
 95 100  
 Leu Thr Gly Leu Trp Val Ile Gly His Glu  
 105 110  
 Cys Gly His His Ala Phe Ser Glu Tyr Gln  
 115 120  
 Leu Ala Asp Asp Ile Val Gly Leu Ile Val  
 125 130  
 His Ser Ala Leu Leu Val Pro Tyr Phe Ser  
 135 140  
 Trp Lys Tyr Ser His Arg Arg His His Ser  
 145 150  
 Asn Ile Gly Ser Leu Glu Arg Asp Glu Val  
 155 160  
 Phe Val Pro Lys Ser Lys Ser Lys Ile Ser  
 165 170  
 Trp Tyr Ser Lys Tyr Ser Asn Asn Pro Pro  
 175 180  
 Gly Arg Val Leu Thr Leu Ala Ala Thr Leu  
 185 190

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Leu Leu Gly Trp Pro Leu Tyr Leu Ala Phe  
 195 200  
 Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe  
 205 210  
 Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile  
 215 220  
 Phe Ser Glu Arg Glu Arg Leu Gln Ile Tyr  
 225 230  
 Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr  
 235 240  
 Phe Val Leu Tyr Gln Ala Thr Met Ala Lys  
 245 250  
 Gly Leu Ala Trp Val Met Arg Ile Tyr Gly  
 255 260  
 Val Pro Leu Leu Ile Val Asn Cys Phe Leu  
 265 270  
 Val Met Ile Thr Tyr Leu Gln His Thr His  
 275 280  
 Pro Ala Ile Pro Arg Tyr Gly Ser Ser Glu  
 285 290  
 Trp Asp Trp Leu Arg Gly Ala Met Val Thr  
 295 300  
 Val Asp Arg Asp Tyr Gly Val Leu Asn Lys  
 305 310  
 Val Phe His Asn Ile Ala Asp Thr His Val  
 315 320  
 Ala His His Leu Phe Ala Thr Val Pro His  
 325 330  
 Tyr His Ala Met Glu Ala Thr Lys Ala Ile  
 335 340  
 Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr  
 345 350  
 Asp Gly Thr Pro Phe Tyr Lys Ala Leu Trp  
 355 360

Sub  
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Ala	Phe	Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp
				115					120
Thr	Val	Gly	Leu	Ile	Phe	His	Ser	Phe	Leu
				125					130
Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser
				135					140
His	Arg	Arg	His	His	Ser	Asn	Thr	Gly	Ser
				145					150
Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys
				155					160
Gln	Lys	Ser	Ala	Ile	Lys	Trp	Tyr	Gly	Lys
				165					170
Tyr	Leu	Asn	Asn	Pro	Leu	Gly	Arg	Ile	Met
				175					180
Met	Leu	Thr	Val	Gln	Phe	Val	Leu	Gly	Trp
				185					190
Pro	Leu	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly
				195					200
Arg	Pro	Tyr	Asp	Gly	Phe	Ala	Cys	His	Phe
				205					210
Phe	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg
				215					220
Glu	Arg	Leu	Gln	Ile	Tyr	Leu	Ser	Asp	Ala
				225					230
Gly	Ile	Leu	Ala	Val	Cys	Phe	Gly	Leu	Tyr
				235					240
Arg	Tyr	Ala	Ala	Ala	Gln	Gly	Met	Ala	Ser
				245					250
Met	Ile	Cys	Leu	Tyr	Gly	Val	Pro	Leu	Leu
				255					260
Ile	Val	Asn	Ala	Phe	Leu	Val	Leu	Ile	Thr
				265					270
Tyr	Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro
				275					280

q <sup>1</sup>	q <sup>2</sup>	q <sup>3</sup>	q <sup>4</sup>	q <sup>5</sup>	q <sup>6</sup>	q <sup>7</sup>	q <sup>8</sup>	q <sup>9</sup>	q <sup>10</sup>	q <sup>11</sup>	q <sup>12</sup>	q <sup>13</sup>	q <sup>14</sup>	q <sup>15</sup>	q <sup>16</sup>	q <sup>17</sup>	q <sup>18</sup>	q <sup>19</sup>	q <sup>20</sup>	q <sup>21</sup>	q <sup>22</sup>	q <sup>23</sup>	q <sup>24</sup>	q <sup>25</sup>	q <sup>26</sup>	q <sup>27</sup>	q <sup>28</sup>	q <sup>29</sup>	q <sup>30</sup>	q <sup>31</sup>	q <sup>32</sup>	q <sup>33</sup>	q <sup>34</sup>	q <sup>35</sup>	q <sup>36</sup>	q <sup>37</sup>	q <sup>38</sup>	q <sup>39</sup>	q <sup>40</sup>	q <sup>41</sup>	q <sup>42</sup>	q <sup>43</sup>	q <sup>44</sup>	q <sup>45</sup>	q <sup>46</sup>	q <sup>47</sup>	q <sup>48</sup>	q <sup>49</sup>	q <sup>50</sup>	q <sup>51</sup>	q <sup>52</sup>	q <sup>53</sup>	q <sup>54</sup>	q <sup>55</sup>	q <sup>56</sup>	q <sup>57</sup>	q <sup>58</sup>	q <sup>59</sup>	q <sup>60</sup>	q <sup>61</sup>	q <sup>62</sup>	q <sup>63</sup>	q <sup>64</sup>	q <sup>65</sup>	q <sup>66</sup>	q <sup>67</sup>	q <sup>68</sup>	q <sup>69</sup>	q <sup>70</sup>	q <sup>71</sup>	q <sup>72</sup>	q <sup>73</sup>	q <sup>74</sup>	q <sup>75</sup>	q <sup>76</sup>	q <sup>77</sup>	q <sup>78</sup>	q <sup>79</sup>	q <sup>80</sup>	q <sup>81</sup>	q <sup>82</sup>	q <sup>83</sup>	q <sup>84</sup>	q <sup>85</sup>	q <sup>86</sup>	q <sup>87</sup>	q <sup>88</sup>	q <sup>89</sup>	q <sup>90</sup>	q <sup>91</sup>	q <sup>92</sup>	q <sup>93</sup>	q <sup>94</sup>	q <sup>95</sup>	q <sup>96</sup>	q <sup>97</sup>	q <sup>98</sup>	q <sup>99</sup>	q <sup>100</sup>	q <sup>101</sup>	q <sup>102</sup>	q <sup>103</sup>	q <sup>104</sup>	q <sup>105</sup>	q <sup>106</sup>	q <sup>107</sup>	q <sup>108</sup>	q <sup>109</sup>	q <sup>110</sup>	q <sup>111</sup>	q <sup>112</sup>	q <sup>113</sup>	q <sup>114</sup>	q <sup>115</sup>	q <sup>116</sup>	q <sup>117</sup>	q <sup>118</sup>	q <sup>119</sup>	q <sup>120</sup>	q <sup>121</sup>	q <sup>122</sup>	q <sup>123</sup>	q <sup>124</sup>	q <sup>125</sup>	q <sup>126</sup>	q <sup>127</sup>	q <sup>128</sup>	q <sup>129</sup>	q <sup>130</sup>	q <sup>131</sup>	q <sup>132</sup>	q <sup>133</sup>	q <sup>134</sup>	q <sup>135</sup>	q <sup>136</sup>	q <sup>137</sup>	q <sup>138</sup>	q <sup>139</sup>	q <sup>140</sup>	q <sup>141</sup>	q <sup>142</sup>	q <sup>143</sup>	q <sup>144</sup>	q <sup>145</sup>	q <sup>146</sup>	q <sup>147</sup>	q <sup>148</sup>	q <sup>149</sup>	q <sup>150</sup>	q <sup>151</sup>	q <sup>152</sup>	q <sup>153</sup>	q <sup>154</sup>	q <sup>155</sup>	q <sup>156</sup>	q <sup>157</sup>	q <sup>158</sup>	q <sup>159</sup>	q <sup>160</sup>	q <sup>161</sup>	q <sup>162</sup>	q <sup>163</sup>	q <sup>164</sup>	q <sup>165</sup>	q <sup>166</sup>	q <sup>167</sup>	q <sup>168</sup>	q <sup>169</sup>	q <sup>170</sup>	q <sup>171</sup>	q <sup>172</sup>	q <sup>173</sup>	q <sup>174</sup>	q <sup>175</sup>	q <sup>176</sup>	q <sup>177</sup>	q <sup>178</sup>	q <sup>179</sup>	q <sup>180</sup>	q <sup>181</sup>	q <sup>182</sup>	q <sup>183</sup>	q <sup>184</sup>	q <sup>185</sup>	q <sup>186</sup>	q <sup>187</sup>	q <sup>188</sup>	q <sup>189</sup>	q <sup>190</sup>	q <sup>191</sup>	q <sup>192</sup>	q <sup>193</sup>	q <sup>194</sup>	q <sup>195</sup>	q <sup>196</sup>	q <sup>197</sup>	q <sup>198</sup>	q <sup>199</sup>	q <sup>200</sup>	q <sup>201</sup>	q <sup>202</sup>	q <sup>203</sup>	q <sup>204</sup>	q <sup>205</sup>	q <sup>206</sup>	q <sup>207</sup>	q <sup>208</sup>	q <sup>209</sup>	q <sup>210</sup>	q <sup>211</sup>	q <sup>212</sup>	q <sup>213</sup>	q <sup>214</sup>	q <sup>215</sup>	q <sup>216</sup>	q <sup>217</sup>	q <sup>218</sup>	q <sup>219</sup>	q <sup>220</sup>	q <sup>221</sup>	q <sup>222</sup>	q <sup>223</sup>	q <sup>224</sup>	q <sup>225</sup>	q <sup>226</sup>	q <sup>227</sup>	q <sup>228</sup>	q <sup>229</sup>	q <sup>230</sup>	q <sup>231</sup>	q <sup>232</sup>	q <sup>233</sup>	q <sup>234</sup>	q <sup>235</sup>	q <sup>236</sup>	q <sup>237</sup>	q <sup>238</sup>	q <sup>239</sup>	q <sup>240</sup>	q <sup>241</sup>	q <sup>242</sup>	q <sup>243</sup>	q <sup>244</sup>	q <sup>245</sup>	q <sup>246</sup>	q <sup>247</sup>	q <sup>248</sup>	q <sup>249</sup>	q <sup>250</sup>	q <sup>251</sup>	q <sup>252</sup>	q <sup>253</sup>	q <sup>254</sup>	q <sup>255</sup>	q <sup>256</sup>	q <sup>257</sup>	q <sup>258</sup>	q <sup>259</sup>	q <sup>260</sup>	q <sup>261</sup>	q <sup>262</sup>	q <sup>263</sup>	q <sup>264</sup>	q <sup>265</sup>	q <sup>266</sup>	q <sup>267</sup>	q <sup>268</sup>	q <sup>269</sup>	q <sup>270</sup>	q <sup>271</sup>	q <sup>272</sup>	q <sup>273</sup>	q <sup>274</sup>	q <sup>275</sup>	q <sup>276</sup>	q <sup>277</sup>	q <sup>278</sup>	q <sup>279</sup>	q <sup>280</sup>	q <sup>281</sup>	q <sup>282</sup>	q <sup>283</sup>	q <sup>284</sup>	q <sup>285</sup>	q <sup>286</sup>	q <sup>287</sup>	q <sup>288</sup>	q <sup>289</sup>	q <sup>290</sup>	q <sup>291</sup>	q <sup>292</sup>	q <sup>293</sup>	q <sup>294</sup>	q <sup>295</sup>	q <sup>296</sup>	q <sup>297</sup>	q <sup>298</sup>	q <sup>299</sup>	q <sup>300&lt;/</sup>
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His Tyr Asp Ser Ser Glu Trp Asp Trp Leu  
 285 290  
 Arg Gly Ala Leu Ala Thr Val Asp Arg Asp  
 295 300  
 Tyr Gly Ile Leu Asn Lys Val Phe His Asn  
 305 310  
 Ile Thr Asp Thr His Val Ala His His Leu  
 315 320  
 Phe Ser Thr Met Pro His Tyr Asn Ala Met  
 325 330  
 Glu Ala Thr Lys Ala Ile Lys Pro Ile Leu  
 335 340  
 Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro  
 345 350  
 Trp Tyr Val Ala Met Tyr Arg Glu Ala Lys  
 355 360  
 Glu Cys Ile Tyr Val Glu Pro Asp Arg Glu  
 365 370  
 Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn  
 375 380  
 Asn Lys Leu

## (2) INFORMATION FOR SEQ ID NO:7

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gly Ala Gly Gly Arg Met Gln Val Ser  
 5 10  
 Pro Pro Ser Lys Lys Ser Glu Thr Asp Asn  
 15 20  
 Ile Lys Arg Val Pro Cys Glu Thr Pro Pro  
 25 30

Sub  
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Phe Thr Val Gly Glu Leu Lys Lys Ala Ile  
 35 40  
 Pro Pro His Cys Phe Lys Arg Ser Ile Pro  
 45 50  
 Arg Ser Phe Ser His Leu Ile Trp Asp Ile  
 55 60  
 Ile Ile Ala Ser Cys Phe Tyr Tyr Val Ala  
 65 70  
 Thr Thr Tyr Phe Pro Leu Leu Pro Asn Pro  
 75 80  
 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp  
 85 90  
 Ala Cys Gln Gly Cys Val Leu Thr Gly Val  
 95 100  
 Trp Val Ile Ala His Glu Cys Gly His Ala  
 105 110  
 Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp  
 115 120  
 Thr Val Gly Leu Ile Phe His Ser Phe Leu  
 125 130  
 Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser  
 135 140  
 His Arg Arg His His Ser Asn Thr Gly Ser  
 145 150  
 Leu Glu Arg Asp Glu Val Phe Val Pro Arg  
 155 160  
 Arg Ser Gln Thr Ser Ser Gly Thr Ala Ser  
 165 170  
 Thr Ser Thr Thr Phe Gly Arg Thr Val Met  
 175 180  
 Leu Thr Val Gln Phe Thr Leu Gly Trp Pro  
 185 190  
 Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg  
 195 200

Sub  
 at  
 cont

Sub  
at  
cont

Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn  
375 380

Asn Lys Leu Xaa

(2) INFORMATION FOR SEQ ID NO:8

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Leu Leu Thr Ser Phe Ser Tyr Val Val  
5 10

Tyr Asp Leu Ser Phe Ala Phe Ile Phe Tyr  
15 20

Ile Ala Thr Thr Tyr Phe His Leu Leu Pro  
25 30

Gln Pro Phe Ser Leu Ile Ala Trp Pro Ile  
35 40

Tyr Trp Val Leu Gln Gly Cys Leu Leu Thr  
45 50

Arg Val Cys Gly His His Ala Phe Ser Lys  
55 60

Tyr Gln Trp Val Asp Asp Val Val Gly Leu  
65 70

Thr Leu His Ser Thr Leu Leu Val Pro Tyr  
75 80

Phe Ser Trp Lys Ile Ser His Arg Arg His  
85 90

His Ser Asn Thr Gly Ser Leu Asp Arg Asp  
95 100

Glu Arg Val Lys Val Ala Trp Phe Ser Lys  
105 110

Tyr Leu Asn Asn Pro Leu Gly Arg Ala Val  
115 120

Sequence

*Sub  
at  
cont*

Ser Leu Leu Val Thr Leu Thr Ile Gly Trp  
 125 130  
 Pro Met Tyr Leu Ala Phe Asn Val Ser Gly  
 135 140  
 Arg Pro Tyr Asp Ser Phe Ala Ser His Tyr  
 145 150  
 His Pro Tyr Arg Val Arg Leu Leu Ile Tyr  
 155 160  
 Val Ser Asp Val Ala Leu Phe Ser Val Thr  
 165 170  
 Tyr Ser Leu Tyr Arg Val Ala Thr Leu Lys  
 175 180  
 Gly Leu Val Trp Leu Leu Cys Val Tyr Gly  
 185 190  
 Val Pro Leu Leu Ile Val Asn Gly Phe Leu  
 195 200  
 Val Thr Ile Thr Tyr Leu Arg Val His Tyr  
 205 210  
 Asp Ser Ser Glu Trp Asp Trp Leu Lys Gly  
 215 220  
 Ala Leu Ala Thr Met Asp Arg Asp Tyr Gly  
 225 230  
 Ile Leu Asn Lys Val Phe His His Ile Thr  
 235 240  
 Asp Thr His Val Ala His His Leu Phe Ser  
 245 250  
 Thr Met Pro His Tyr His Leu Arg Val Lys  
 255 260  
 Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp  
 265 270  
 Asp Thr Pro Phe Tyr Lys Ala Leu Trp Arg  
 275 280  
 Glu Ala Arg Glu Cys Leu Tyr Val Glu Pro  
 285 290

Sub  
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Asp Glu Gly Thr Ser Glu Lys Gly Val Tyr  
295 300

Trp Tyr Arg Asn Lys Tyr Leu Arg Val  
305

(2) INFORMATION FOR SEQ ID NO:9

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Phe Ser Tyr Val Val Tyr Asp Leu Thr Ile  
5 10

Ala Phe Cys Leu Tyr Tyr Val Ala Thr His  
15 20

Tyr Phe His Leu Leu Pro Gly Pro Leu Ser  
25 30

Phe Arg Gly Met Ala Ile Tyr Trp Ala Val  
35 40

Gln Gly Cys Ile Leu Thr Gly Val Trp Val  
45 50

Val Ala Phe Ser Asp Tyr Gln Leu Leu Asp  
55 60

Asp Ile Val Gly Leu Ile Leu His Ser Ala  
65 70

Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr  
75 80

Ser His Arg Arg His His Ser Asn Thr Gly  
85 90

Ser Leu Glu Arg Asp Glu Val Phe Val Pro  
95 100

Lys Val Ser Lys Tyr Leu Asn Asn Pro Pro  
105 110

Gly Arg Val Leu Thr Leu Ala Val Thr Leu  
115 120

Sub  
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Thr Leu Gly Trp Pro Leu Tyr Leu Ala Leu  
 125 130  
 Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe  
 135 140  
 Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile  
 145 150  
 Tyr Ser Val Ile Ser Asp Ala Gly Val Leu  
 155 160  
 Ala Val Val Tyr Gly Leu Phe Arg Leu Ala  
 165 170  
 Met Ala Lys Gly Leu Ala Trp Val Val Cys  
 175 180  
 Val Tyr Gly Val Pro Leu Leu Val Val Asn  
 185 190  
 Gly Phe Leu Val Leu Ile Thr Phe Leu Gln  
 195 200  
 His Thr His Val Ser Glu Trp Asp Trp Leu  
 205 210  
 Arg Gly Ala Leu Ala Thr Val Asp Arg Asp  
 215 220  
 Tyr Gly Ile Leu Asn Lys Val Phe His Asn  
 225 230  
 Ile Thr Asp Thr His Val Ala His His Leu  
 235 240  
 Phe Ser Thr Met Pro His Tyr His Ala Met  
 245 250  
 Glu Ala Thr Val Glu Tyr Tyr Arg Phe Asp  
 255 260  
 Glu Thr Pro Phe Val Lys Ala Met Trp Arg  
 265 270  
 Glu Ala Arg Glu Cys Ile Tyr Val Glu Pro  
 275 280  
 Asp Gln Ser Thr Glu Ser Lys Gly Val Phe  
 285 290

Sub  
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Trp Tyr Asn Asn Lys Leu Ala Met Glu Ala  
295 300

Thr Val

(2) INFORMATION FOR SEQ ID NO:10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Gly Ala Gly Gly Arg Met Thr Glu Lys  
5 10

Glu Arg Glu Lys Gln Glu Gln Leu Ala Arg  
15 20

Ala Thr Gly Gly Ala Ala Met Gln Arg Ser  
25 30

Pro Val Glu Lys Pro Pro Phe Thr Leu Gly  
35 40

Gln Ile Lys Lys Ala Ile Pro Pro His Cys  
45 50

Phe Glu Arg Ser Val Leu Lys Ser Phe Ser  
55 60

Tyr Val Val His Asp Leu Val Ile Ala Ala  
65 70

Ala Leu Leu Tyr Phe Ala Leu Ala Ile Ile  
75 80

Pro Ala Leu Pro Ser Pro Leu Arg Tyr Ala  
85 90

Ala Trp Pro Leu Tyr Trp Ile Ala Gln Gly  
95 100

Ala Phe Ser Asp Tyr Ser Leu Leu Asp Asp  
105 110

Val Val Gly Leu Val Leu His Ser Ser Leu  
115 120

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Met Val Pro Tyr Phe Ser Trp Lys Tyr Ser  
 125 130  
 His Arg Arg His His Ser Asn Thr Gly Ser  
 135 140  
 Leu Glu Arg Asp Glu Val Phe Val Pro Lys  
 145 150  
 Lys Lys Glu Ala Leu Pro Trp Tyr Thr Pro  
 155 160  
 Tyr Val Tyr Asn Asn Pro Val Gly Arg Val  
 165 170  
 Val His Ile Val Val Gln Leu Thr Leu Gly  
 175 180  
 Trp Pro Leu Tyr Leu Ala Thr Asn Ala Ser  
 185 190  
 Gly Arg Pro Tyr Pro Arg Phe Ala Cys His  
 195 200  
 Phe Asp Pro Tyr Gly Pro Ile Tyr Asn Asp  
 205 210  
 Arg Glu Arg Ala Gln Ile Phe Val Ser Asp  
 215 220  
 Ala Gly Val Val Ala Val Ala Phe Gly Leu  
 225 230  
 Tyr Lys Leu Ala Ala Ala Phe Gly Val Trp  
 235 240  
 Trp Val Val Arg Val Tyr Ala Val Pro Leu  
 245 250  
 Leu Ile Val Asn Ala Trp Leu Val Leu Ile  
 255 260  
 Thr Tyr Leu Gln His Thr His Pro Ser Leu  
 265 270  
 Pro His Tyr Asp Ser Ser Glu Trp Asp Trp  
 275 280  
 Leu Arg Gly Ala Leu Ala Thr Met Asp Arg  
 285 290

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Asp Tyr Gly Ile Leu Asn Arg Val Phe His  
 295 300  
 Asn Ile Thr Asp Thr His Val Ala His His  
 305 310  
 Leu Phe Ser Thr Met Pro His Tyr His Ala  
 315 320  
 Met Glu Ala Thr Lys Ala Ile Arg Pro Ile  
 325 330  
 Leu Gly Asp Tyr Tyr His Phe Asp Pro Thr  
 335 340  
 Pro Val Ala Lys Ala Thr Trp Arg Glu Ala  
 345 350  
 Gly Glu Cys Ile Tyr Val Glu Pro Glu Asp  
 355 360  
 Arg Lys Gly Val Phe Trp Tyr Asn Lys Lys  
 365 370  
 Phe Xaa

## (2) INFORMATION FOR SEQ ID NO:11

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Trp Val Met Ala His Asp Cys Gly His His  
 5 10  
 Ala Phe Ser Asp Tyr Gln Leu Leu Asp Asp  
 15 20  
 Val Val Gly Leu Ile Leu His Ser Cys Leu  
 25 30  
 Leu Val Pro Tyr Phe Ser Trp Lys His Ser  
 35 40  
 His Arg Arg His His Ser Asn Thr Gly Ser  
 45 50

Sub  
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Leu Glu Arg Asp Glu Val Phe Val Pro Lys  
 55 60  
 Lys Lys Ser Ser Ile Arg Trp Tyr Ser Lys  
 65 70  
 Tyr Leu Asn Asn Pro Pro Gly Arg Ile Met  
 75 80  
 Thr Ile Ala Val Thr Leu Ser Leu Gly Trp  
 85 90  
 Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly  
 95 100  
 Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr  
 105 110  
 Asp Pro Tyr Gly Pro Ile Tyr Asn Asp Arg  
 115 120  
 Glu Arg Ile Glu Ile Phe Ile Ser Asp Ala  
 125 130  
 Gly Val Leu Ala Val Thr Phe Gly Leu Tyr  
 135 140  
 Gln Leu Ala Ile Ala Lys Gly Leu Ala Trp  
 145 150  
 Val Val Cys Val Tyr Gly Val Pro Leu Leu  
 155 160  
 Val Val Asn Ser Phe Leu Val Leu Ile Thr  
 165 170  
 Phe Leu Gln His Thr His Pro Ala Leu Pro  
 175 180  
 His Tyr Asp Ser Ser Glu Trp Asp Trp Leu  
 185 190  
 Arg Gly Ala Leu Ala Thr Val Asp Arg Asp  
 195 200  
 Tyr Gly Ile Leu Asn Lys Val Phe His Asn  
 205 210  
 Ile Thr Asp Thr Gln Val Ala His His Leu  
 215 220

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Phe Thr Met Pro

(2) INFORMATION FOR SEQ ID NO:12

(i) ~~SEQUENCE~~ CHARACTERISTICS:

- (A) LENGTH: 20 nucleotides  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) ~~SEQUENCE DESCRIPTION:~~ SEQ ID NO:12:

GCTCTTTTGT GCGCTCATTC

20

(2) INFORMATION FOR SEQ ID NO:13

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 nucleotides  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGGTACCAGA AAAGGCCTTG

20

(2) INFORMATION FOR SEQ ID NO:14

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 nucleotides  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TAYWSNCAYM GNMGNCA YCA

20

(2) INFORMATION FOR SEQ ID NO:15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 nucleotides  
(B) TYPE: nucleotide  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

RTGRTGNGCN ACRTGNGTRT C

21

[illegible]

Sub  
at  
cont.